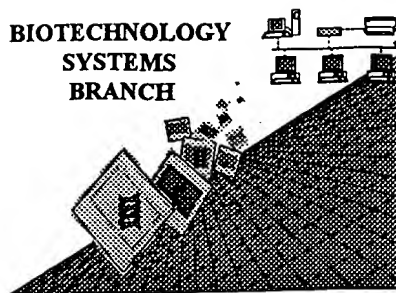


Nicks

RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



P#8

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/451,739A

Source: 1642

Date Processed by STIC: 7/12/2000

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THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY
EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER,
703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

1642

RAW SEQUENCE LISTING DATE: 07/12/2000
 PATENT APPLICATION: US/09/451,739A TIME: 15:56:26

Input Set : A:\lud-5615.txt
 Output Set: N:\CRF3\07122000\I451739A.raw

1 <110> APPLICANT: Jager, Dirk
 2 Scanlan, Matthew
 3 Gure, Ali
 4 Jager, Elke
 5 Knuth, Alexander
 6 Old, Lloyd
 7 Chen, Yao-tseng
 9 <120> TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer Associated Antigens,
 10 the Antigens per se, and Uses Thereof
 12 <130> FILE REFERENCE: LUD 5615
 14 <140> CURRENT APPLICATION NUMBER: 09/451,739A
 16 <141> CURRENT FILING DATE: 1999-11-30
 18 <160> NUMBER OF SEQ ID NOS: 19

Does Not Comply
 Corrected Diskette Needed

ERRORED SEQUENCES

527 <210> SEQ ID NO: 16
 528 <211> LENGTH: 528
 529 <212> TYPE: PRT
 530 <213> ORGANISM: Homo sapiens
 531 <220> FEATURE:
 532 <400> SEQUENCE: 16
 533 Met Lys Val Ser Ile Pro Thr Lys Ala Leu Glu Leu Met Asp Met Gln
 534 1 5 10 15
 536 Thr Phe Lys Ala Glu Pro Pro Glu Lys Pro Ser Ala Phe Glu Pro Ala
 537 20 25 30
 539 Ile Glu Met Gln Lys Ser Val Pro Asn Lys Ala Leu Glu Leu Lys Asn
 540 35 40 45
 542 Glu Gln Thr Leu Arg Ala Asp Glu Ile Leu Pro Ser Glu Ser Lys Gln
 543 50 55 60
 545 Lys Asp Tyr Glu Glu Ser Ser Trp Asp Ser Glu Ser Leu Cys Glu Thr
 546 65 70 75 80
 548 Val Ser Gln Lys Asp Val Cys Leu Pro Lys Ala Thr His Gln Lys Glu
 549 85 90 95
 551 Ile Asp Lys Ile Asn Gly Lys Leu Glu Glu Ser Pro Asp Asn Asp Gly
 552 100 105 110
 554 Phe Leu Lys Ala Pro Cys Arg Met Lys Val Ser Ile Pro Thr Lys Ala
 555 115 120 125
 557 Leu Glu Leu Met Asp Met Gln Thr Phe Lys Ala Glu Pro Pro Glu Lys
 558 130 135 140
 560 Pro Ser Ala Phe Glu Pro Ala Ile Glu Met Gln Lys Ser Val Pro Asn
 561 145 150 155 160
 563 Lys Ala Leu Glu Leu Lys Asn Glu Gln Thr Leu Arg Ala Asp Gln Met
 564 165 170 175
 566 Phe Pro Ser Glu Ser Lys Gln Lys Lys Val Glu Glu Asn Ser Trp Asp
 567 180 185 190

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RAW SEQUENCE LISTING

DATE: 07/12/2000

PATENT APPLICATION: US/09/451,739A

TIME: 15:56:26

Input Set : A:\lud-5615.txt

Output Set: N:\CRF3\07122000\I451739A.raw

```

569 Ser Glu Ser Leu Arg Glu Thr Val Ser Gln Lys Asp Val Cys Val Pro
570      195      200      205
572 Lys Ala Thr His Gln Lys Glu Met Asp Lys Ile Ser Gly Lys Leu Glu
573      210      215      220
575 Asp Ser Thr Ser Leu Ser Lys Ile Leu Asp Thr Val His Ser Cys Glu
576 225      230      235      240
578 Arg Ala Arg Glu Leu Gln Lys Asp His Cys Glu Gln Arg Thr Gly Lys
E--> 579      245      250      255
581 Met Glu Gln Met Lys Lys Phe Cys Val Leu Lys Lys Lys Leu Ser
E--> 582      260      265      270
584 Glu Ala Lys Glu Ile Lys Ser Gln Leu Glu Asn Gln Lys Val Lys Trp
E--> 585      275      280      285
587 Glu Gln Glu Leu Cys Ser Val Arg Leu Thr Leu Asn Gln Glu Glu Glu
E--> 588 305      310      315      320
590 Lys Arg Arg Asn Ala Asp Ile Leu Asn Glu Lys Ile Arg Glu Glu Leu
E--> 591      325      330      335
593 Gly Arg Ile Glu Glu Gln His Arg Lys Glu Leu Glu Val Lys Gln Gln
E--> 594      340      345      350
596 Leu Glu Gln Ala Leu Arg Ile Gln Asp Ile Glu Leu Lys Ser Val Glu
E--> 597      355      360      365
599 Ser Asn Leu Asn Gln Val Ser His Thr His Glu Asn Glu Asn Tyr Leu
E--> 600      370      375      380
602 Leu His Glu Asn Cys Met Leu Lys Lys Glu Ile Ala Met Leu Lys Leu
E--> 603 385      390      395      400
605 Glu Ile Ala Thr Leu Lys His Gln Tyr Gln Glu Lys Glu Asn Lys Tyr
E--> 606      405      410      415
608 Phe Glu Asp Ile Lys Ile Leu Lys Glu Lys Asn Ala Glu Leu Gln Met
E--> 609      420      425      430
611 Thr Leu Lys Leu Lys Glu Glu Ser Leu Thr Lys Arg Ala Ser Gln Tyr
E--> 612      435      440      445
614 Ser Gly Gln Leu Lys Val Leu Ile Ala Glu Asn Thr Met Leu Thr Ser
E--> 615      450      455      460
617 Lys Leu Lys Glu Lys Gln Asp Lys Glu Ile Leu Glu Ala Glu Ile Glu
E--> 618 465      470      475      480
620 Ser His His Pro Arg Leu Ala Ser Ala Val Gln Asp His Asp Gln Ile
E--> 621      485      490      495
623 Val Thr Ser Arg Lys Ser Gln Glu Pro Ala Phe His Ile Ala Gly Asp
E--> 624      500      505      510
626 Ala Cys Leu Gln Arg Lys Met Asn Val Asp Val Ser Ser Thr Asp Ile
E--> 627      515      520      525

```

numbering off

↓

FSI

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

DATE: 07/12/2000

PATENT APPLICATION: US/09/451,739A

TIME: 15:56:27

Input Set : A:\lud-5615.txt

Output Set: N:\CRF3\07122000\I451739A.raw

L:25 M:283 W: Missing Blank Line separator, <220> field identifier
L:28 M:283 W: Missing Blank Line separator, <400> field identifier
L:35 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:35 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:1
L:86 M:283 W: Missing Blank Line separator, <220> field identifier
L:87 M:283 W: Missing Blank Line separator, <400> field identifier
L:133 M:283 W: Missing Blank Line separator, <220> field identifier
L:134 M:283 W: Missing Blank Line separator, <400> field identifier
L:166 M:283 W: Missing Blank Line separator, <220> field identifier
L:167 M:283 W: Missing Blank Line separator, <400> field identifier
L:203 M:283 W: Missing Blank Line separator, <220> field identifier
L:204 M:283 W: Missing Blank Line separator, <400> field identifier
L:264 M:283 W: Missing Blank Line separator, <220> field identifier
L:265 M:283 W: Missing Blank Line separator, <400> field identifier
L:313 M:283 W: Missing Blank Line separator, <220> field identifier
L:314 M:283 W: Missing Blank Line separator, <400> field identifier
L:365 M:283 W: Missing Blank Line separator, <220> field identifier
L:368 M:283 W: Missing Blank Line separator, <400> field identifier
L:391 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8
L:391 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:8
L:400 M:283 W: Missing Blank Line separator, <220> field identifier
L:401 M:283 W: Missing Blank Line separator, <400> field identifier
L:409 M:283 W: Missing Blank Line separator, <220> field identifier
L:410 M:283 W: Missing Blank Line separator, <400> field identifier
L:418 M:283 W: Missing Blank Line separator, <220> field identifier
L:419 M:283 W: Missing Blank Line separator, <400> field identifier
L:427 M:283 W: Missing Blank Line separator, <220> field identifier
L:428 M:283 W: Missing Blank Line separator, <400> field identifier
L:436 M:283 W: Missing Blank Line separator, <220> field identifier
L:437 M:283 W: Missing Blank Line separator, <400> field identifier
L:445 M:283 W: Missing Blank Line separator, <220> field identifier
L:446 M:283 W: Missing Blank Line separator, <400> field identifier
L:454 M:283 W: Missing Blank Line separator, <220> field identifier
L:457 M:283 W: Missing Blank Line separator, <400> field identifier
L:512 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15
L:512 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:15
L:516 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15
L:516 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:15
L:520 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15
L:520 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:15
L:522 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15
L:522 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:15
L:524 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15
L:524 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:15
L:531 M:283 W: Missing Blank Line separator, <220> field identifier
L:532 M:283 W: Missing Blank Line separator, <400> field identifier
L:579 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
L:582 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16

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VERIFICATION SUMMARY

DATE: 07/12/2000

PATENT APPLICATION: US/09/451,739A

TIME: 15:56:27

Input Set : A:\lud-5615.txt

Output Set: N:\CRF3\07122000\I451739A.raw

L:585 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
L:588 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
L:591 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
L:594 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
L:597 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
L:600 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
L:603 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
L:606 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
L:609 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
L:612 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
L:615 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
L:618 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
L:621 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
L:624 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
L:627 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
L:627 M:252 E: No. of Seq. differs, <211>LENGTH:Input:528 Found:512 SEQ:16
L:634 M:283 W: Missing Blank Line separator, <220> field identifier
L:635 M:283 W: Missing Blank Line separator, <400> field identifier
L:643 M:283 W: Missing Blank Line separator, <220> field identifier
L:644 M:283 W: Missing Blank Line separator, <400> field identifier
L:652 M:283 W: Missing Blank Line separator, <220> field identifier
L:653 M:283 W: Missing Blank Line separator, <400> field identifier